

CRF Errors Corrected by the STIC Systems Branch

CRF Processing Date: 5/15/2002

Edited by: [Signature]

Verified by: [Signature]

Serial Number: 09/970,517C

ENTERED

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JUN 04 2002
TECHNICAL CENTER 1600/2400
1645

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form. 3/1/95



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JUN 04 2002

TECH CENTER 1600/2900

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/770,517C

DATE: 05/14/2002
TIME: 18:29:08

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\05142002\I770517C.raw

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4 <110> APPLICANT: Mitsuhashi, Kazuya
5     Yamamoto, Hiroaki
6     Matsuyama, Akinobu
7     Tokuyama, Shinji
9 <120> TITLE OF INVENTION: D-AMINOACYLASE AND GENE ENCODING THE SAME
11 <130> FILE REFERENCE: 06501-072001
13 <140> CURRENT APPLICATION NUMBER: US 09/770,517C
14 <141> CURRENT FILING DATE: 2001-01-26
16 <150> PRIOR APPLICATION NUMBER: JP 2000-019080
17 <151> PRIOR FILING DATE: 2000-01-27
19 <150> PRIOR APPLICATION NUMBER: JP 2000-150578
20 <151> PRIOR FILING DATE: 2000-05-22
22 <160> NUMBER OF SEQ ID NOS: 27
24 <170> SOFTWARE: PatentIn Ver. 2.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 1677
28 <212> TYPE: DNA
29 <213> ORGANISM: Hypomyces mycophilus
31 <400> SEQUENCE: 1
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33 ccctttgtgg ccgatgtgct ggtttogaag ggactgattg ccaagattgg taaccccggt 120
34 tccatcaatg caactccaga tacgcggcat ctgcagctca caggctacat tctatctcct 180
35 ggtttcatcg atatgcatgc gcattcagac ctctacctac tctctcatcc tgaccacgag 240
36 gccaaaatca cccaaggatg cacaacggaa gttgtgggcc aagacgggat atcatatgca 300
37 ccaattcgta atgtagacca gttgagggcg atccgagaac agattgctgg atggaatggc 360
38 aatcctacag atgaggagtg ccggacaact ctcaaaggcg ttggcatgtt tgaatggcag 420
39 actattgggg aatacttgga ttgtttggag agaaacagga cggccactaa tgcgccatg 480
40 ttggttccgc aaggcaacct gagattattg gcatgtggcc catacgatac tccagcatct 540
41 gcagaagaga ttcaagatca aatccagctc ttgcgagagg ctatggctca gggtgctgtc 600
42 gggatgtcta gtggtctcac ttatacacc ccgcatgtatg cttccacgtc ggaactagct 660
43 tctctgtgcg cggccctcgc acaagaattt ccaggtgcat tctatgcgcc acatcataga 720
44 agttatgggt tccaggccat cgaaagtatt gccgaaatgt tggatctcgg agagtcaaca 780
45 ggctgtccca ttcattctac acatgcaacg ctcaactttt cagaaaataa gggtaaagct 840
46 cctgtcctca tctctatggt tgataaatct cttgctgcag gcgtggatgt cacacttgat 900
47 acgtatccat acttgccagg ctgtacaact ctggctgcat tgttgccaag ttgggcatct 960
48 gctggcggcc cacaagagac gcttaaaagg cttgaggatg cagaatcgag agaaaagatt 1020
49 cgtatagcgg tggaaatcaa aggggtgtgat ggcggccatg gtattccaac caactgggac 1080
50 gaaatccaga tcgggacgac taatgaacca tcaatcgcat cgtattctgg tcgcaggcta 1140
51 tcagaagtgg cacagtctgt tggaaagccg accatcgagg tctttttcga gattctgcaa 1200
52 aaggataagc tcgcaacgag ctgtatcatg catgttgcca atgaagaaaa cgtccgacag 1260
53 atcatgcagc atcgggtcca tatggcaggc agtgatggga tcttgacagg gcagacgcta 1320
54 caccacgag cttatggcac attcacgagg tatttaggac actattctcg tgaactctcg 1380
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56 gtatatccat atcgcggtct gattgctgaa ggatccgctg cgcacattgt ggtttttaac 1500
57 cccgaaacgg taaaggatat gtcgacgtat gaagagccaa aggtgccaag tcggggcatt 1560
58 agatttgttc tagttaacgg ccagatagct gtggacgaag gcaagatgac aggcacaaga 1620
59 gggggtaaaa cactgagaag aagcaccgat ggcaaggta aggcaagaga tgagtaa 1677
61 <210> SEQ ID NO: 2
62 <211> LENGTH: 558
63 <212> TYPE: PRT
64 <213> ORGANISM: Hypomyces mycophilus
66 <400> SEQUENCE: 2
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68 1 5 10 15
69 Glu Ala Ala Gln Pro Phe Val Ala Asp Val Leu Val Ser Lys Gly Leu
70 20 25 30
71 Ile Ala Lys Ile Gly Asn Pro Gly Ser Ile Asn Ala Thr Pro Asp Thr
72 35 40 45
73 Arg His Leu Asp Val Thr Gly Tyr Ile Leu Ser Pro Gly Phe Ile Asp
74 50 55 60
75 Met His Ala His Ser Asp Leu Tyr Leu Leu Ser His Pro Asp His Glu
76 65 70 75 80
77 Ala Lys Ile Thr Gln Gly Cys Thr Thr Glu Val Val Gly Gln Asp Gly
78 85 90 95
79 Ile Ser Tyr Ala Pro Ile Arg Asn Val Asp Gln Leu Arg Ala Ile Arg
80 100 105 110
81 Glu Gln Ile Ala Gly Trp Asn Gly Asn Pro Thr Asp Glu Glu Cys Arg
82 115 120 125
83 Thr Thr Leu Lys Gly Val Gly Met Phe Glu Trp Gln Thr Ile Gly Glu
84 130 135 140
85 Tyr Leu Asp Cys Leu Glu Arg Asn Arg Thr Ala Thr Asn Val Ala Met
86 145 150 155 160
87 Leu Val Pro Gln Gly Asn Leu Arg Leu Leu Ala Cys Gly Pro Tyr Asp
88 165 170 175
89 Thr Pro Ala Ser Ala Glu Glu Ile Gln Asp Gln Ile Gln Leu Leu Arg
90 180 185 190
91 Glu Ala Met Ala Gln Gly Ala Val Gly Met Ser Ser Gly Leu Thr Tyr
92 195 200 205
93 Thr Pro Gly Met Tyr Ala Ser Thr Ser Glu Leu Ala Ser Leu Cys Ala
94 210 215 220
95 Ala Leu Ala Gln Glu Phe Pro Gly Ala Phe Tyr Ala Pro His His Arg
96 225 230 235 240
97 Ser Tyr Gly Phe Gln Ala Ile Glu Ser Tyr Ala Glu Met Leu Asp Leu
98 245 250 255
99 Gly Glu Ser Thr Gly Cys Pro Ile His Leu Thr His Ala Thr Leu Asn
100 260 265 270
101 Phe Ser Glu Asn Lys Gly Lys Ala Pro Val Leu Ile Ser Met Val Asp
102 275 280 285
103 Lys Ser Leu Ala Ala Gly Val Asp Val Thr Leu Asp Thr Tyr Pro Tyr
104 290 295 300
105 Leu Pro Gly Cys Thr Thr Leu Ala Ala Leu Leu Pro Ser Trp Ala Ser
106 305 310 315 320

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107 Ala Gly Gly Pro Gln Glu Thr Leu Lys Arg Leu Glu Asp Ala Glu Ser
108                               325                               330                               335
109 Arg Glu Lys Ile Arg Ile Ala Val Glu Ile Lys Gly Cys Asp Gly Gly
110                               340                               345                               350
111 His Gly Ile Pro Thr Asn Trp Asp Glu Ile Gln Ile Gly Thr Thr Asn
112                               355                               360                               365
113 Glu Pro Ser Ile Ala Ser Tyr Ser Gly Arg Arg Leu Ser Glu Val Ala
114                               370                               375                               380
115 Gln Ser Val Gly Lys Pro Thr Ile Glu Val Phe Phe Glu Ile Leu Gln
116 385                               390                               395                               400
117 Lys Asp Lys Leu Ala Thr Ser Cys Ile Met His Val Gly Asn Glu Glu
118                               405                               410                               415
119 Asn Val Arg Gln Ile Met Gln His Arg Val His Met Ala Gly Ser Asp
120                               420                               425                               430
121 Gly Ile Leu His Gly Gln Thr Leu His Pro Arg Ala Tyr Gly Thr Phe
122                               435                               440                               445
123 Thr Arg Tyr Leu Gly His Tyr Ser Arg Glu Leu Ser Leu Val Ala Leu
124                               450                               455                               460
125 Pro Ser Met Ile Ala His Leu Thr Ser Arg Pro Ala Lys Arg Leu Ser
126 465                               470                               475                               480
127 Val Tyr Pro Tyr Arg Gly Leu Ile Ala Glu Gly Ser Ala Ala Asp Ile
128                               485                               490                               495
129 Val Val Phe Asn Pro Glu Thr Val Lys Asp Met Ser Thr Tyr Glu Glu
130                               500                               505                               510
131 Pro Lys Val Pro Ser Arg Gly Ile Arg Phe Val Leu Val Asn Gly Gln
132                               515                               520                               525
133 Ile Ala Val Asp Glu Gly Lys Met Thr Gly Thr Arg Gly Gly Lys Thr
134                               530                               535                               540
135 Leu Arg Arg Ser Thr Asp Gly Lys Val Lys Ala Arg Asp Glu
136 545                               550                               555

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138 <210> SEQ ID NO: 3

139 <211> LENGTH: 20

140 <212> TYPE: DNA

141 <213> ORGANISM: Artificial Sequence

143 <220> FEATURE:

144 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence

146 <400> SEQUENCE: 3

147 cccggcttca tcgacatgca

20

149 <210> SEQ ID NO: 4

150 <211> LENGTH: 20

151 <212> TYPE: DNA

152 <213> ORGANISM: Artificial Sequence

154 <220> FEATURE:

155 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence

W--> 157 <221> NAME/KEY: misc_feature

158 <222> LOCATION: 18

159 <223> OTHER INFORMATION: n = A,T,C or G

W--> 161 <400> 4

W--> 162 ttcatcgaca tgcaygcnc

20

RAW SEQUENCE LISTING

DATE: 05/14/2002

PATENT APPLICATION: US/09/770,517C

TIME: 18:29:08

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\05142002\I770517C.raw

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164 <210> SEQ ID NO: 5
165 <211> LENGTH: 20
166 <212> TYPE: DNA
167 <213> ORGANISM: Artificial Sequence
169 <220> FEATURE:
170 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
W--> 172 <221> NAME/KEY: misc_feature
173 <222> LOCATION: 3, 6, 15
174 <223> OTHER INFORMATION: n = A,T,C or G
W--> 176 <400> 5
W--> 177 tgnggngcrt craangcytg 20
179 <210> SEQ ID NO: 6
180 <211> LENGTH: 20
181 <212> TYPE: DNA
182 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
W--> 187 <221> NAME/KEY: misc_feature
188 <222> LOCATION: 3, 9
189 <223> OTHER INFORMATION: n = A,T,C or G
W--> 191 <400> 6
W--> 192 aangcytgng grtaytctc 20
194 <210> SEQ ID NO: 7
195 <211> LENGTH: 321
196 <212> TYPE: DNA
197 <213> ORGANISM: Hypomyces mycophilus
199 <400> SEQUENCE: 7
200 ttcacgcaca tgcacgcgca gctggatggt caaccttgac aactacaaca agatactctc 60
201 tgtagacaaa aaatcggggg tcgtggatcat gcagagcggc attcgactat acaccctttg 120
202 cgaagagctg gagctacatg gcctggcaat gccgaacctg ggcagtataa acgagcaatc 180
203 catcgccggc gccatatcta caggcacaca cggcagcagc atccaccacg gcctcatgtc 240
204 tgaggatatt ctgctctga aaatcactct cgcgggcggc aagacggagg catgctccaa 300
205 agacgaatac ccccaagcct t 321
207 <210> SEQ ID NO: 8
208 <211> LENGTH: 20
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
215 <400> SEQUENCE: 8
216 aggccaaaat caccgaagga 20
218 <210> SEQ ID NO: 9
219 <211> LENGTH: 20
220 <212> TYPE: DNA
221 <213> ORGANISM: Artificial Sequence
223 <220> FEATURE:
224 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
226 <400> SEQUENCE: 9
227 attggggaat acttgattg 20

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\05142002\I770517C.raw

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229 <210> SEQ ID NO: 10
230 <211> LENGTH: 20
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
237 <400> SEQUENCE: 10
238 ctggttcttt ccgcctcaga                                20
240 <210> SEQ ID NO: 11
241 <211> LENGTH: 20
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
248 <400> SEQUENCE: 11
249 attaaccctc actaaagggc                                20
251 <210> SEQ ID NO: 12
252 <211> LENGTH: 1325
253 <212> TYPE: DNA
254 <213> ORGANISM: Hypomyces mycophilus
256 <400> SEQUENCE: 12
257 caggacggcc actaatgtcg ccatgttggt tccgcaaggc aacctgagat tattggcatg    60
258 tggcccatac gatactccag catctgcaga agagattcaa gatcaaatcc agctcttgcg    120
259 agaggctatg gctcagggcg ctgtcgggat gtctagtggc ctcaactata caccggcat    180
260 gtatgcttcc acgtcggaac tagcttctct gtgcgcggcc ctgcgacaag aatttccagg    240
261 tgcattctat gcgccacatc atagaagtta tgggttccag gccatcgaaa gttatgccga    300
262 aatggttgat ctcgagagat caacaggctg tcccattcat cttacacatg caacgctcaa    360
263 cttttcagaa aataagggtg aagctcctgt cctcatctct atggttgata aatctcttgc    420
264 tgcaggcgtg gatgtcacac ttgatacgta tccatacttg ccaggctgta caactctggc    480
265 tgcattgctg ccaagtcggg catctgctgg cggccacaa gagacgctta aaaggcttga    540
266 ggatgcagaa tcgagagaaa agattcgtat agccgtggaa atcaaagggg gtgatggcgg    600
267 ccatggtatt ccaaccaact gggacgaaat ccagatcggg acgactaatg aaccatcaat    660
268 cgcacgtat tctggtcgca ggctatcaga agtggcacag tctgttgaa agccgaccat    720
269 cgaagtcttt ttcgagattc tgcaaaagga taagctcgca acgagctgta tcatgcatgt    780
270 tggcaatgaa gaaaacgtcc gacagatcat gcagcatcgg gtccatatgg caggcagtga    840
271 tgggatcttg cacgggcaga cgctacaccc acgagcttat ggcacattca cgcggtattt    900
272 aggacactat tctcgtgaac tctcgttgt tgcctcgcg tccatgatcg ctcaccttac    960
273 atcacggccc gccaaacgac tttcggtata tccatatcgc ggtctgattg ctgaaggatc   1020
274 cgctgcccga attgtggttt ttaaccccga aacggtaaag gatatgtcga cgtatgaaga   1080
275 gccaaagggtg ccaagtcggg gcattagatt tgttctagtt aacggccaga tagctgtgga   1140
276 cgaaggcaag atgacaggca caagaggggg taaaacactg agaagaagca ccgatggcaa   1200
277 ggtgaaggca agagatgagt aaagtctcga tctgcatccg cgtgcccaac aacaggatca   1260
278 agtcgtcaca gcatgatacg gcaggctttg gagtagatac catgtcatgg gggaaatggg   1320
279 caata                                              1325
281 <210> SEQ ID NO: 13
282 <211> LENGTH: 21
283 <212> TYPE: DNA
284 <213> ORGANISM: Artificial Sequence
286 <220> FEATURE:

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/770,517C

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Input Set : A:\PTO.AMC.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; N Pos. 18
Seq#:5; N Pos. 3,6,15
Seq#:6; N Pos. 3,9